The above protocols are used to develop primers from Sequence id GM_M02_A2_B07_MR_MR containing the following nucleotide composition (SEQ ID NO: 36936):

AGGCGTTTTNCCTTGATACCTTCGNAGGTCCANCCTTTTNCTTGCTGTATCGA
CTCATTAACACCAAGCTCGGTGAGCACTCTGAAGATTATGACAACTTTCGNTG
ATCTTTTTGTCATCGATATTNTAGNAGAGACCAATCTTTCTTCTTCAAATGTCG
CTCATGATATTTATTGTAATTATCTTCAATGTATGTCCAAAAAGTTAACCTTTT
TTGGACCCCCACAATAGAAATCTTTGAAATATTTAGCCATGTGTTGGCAAGCC
ATTCATATTTCTTTGCGGAGAAACATGATCTATTGTGTCTTTCGGATGCTTCTT
CTATGTcttcttcttcttcttcttcttcttcttcttCATTGACCACAATATTATCCAACTCAACTTA
GGTGCAAAATGGTGGAATTTGAGACTTTGACGCANAGTCAGATGGTGCGTCA
TGCTCTTTCATTACATTGGACATCATNTACTACCCTTTGAAGACCCTCGATCC
ATGGAAGGGTTAATTGGTG

This sequence contains CTT dinucleotide repeats with a repeat unit of 11. Using the Primer 3 program, two primers are selected: SER157F GTGTCTTTCGGATGCTTCTTCT (SEQ ID NO: 36937) and SER157R CACCATTTTGCACCTAAGTTGA (SEQ ID NO: 36938). When these two primers are used to amplify genomic DNAs from eight different varieties, Minsoy, Noir, PIC, HS-1, A3244, H6686, A0868 and H5088, three alleles are detected. Sizes of these alleles ranged from 80 to 110 base pairs. The size variation in the PCR products result from repeat numbers in different varieties.

IN THE CLAIMS

Please **cancel** non–elected claims 17 and 18, without prejudice to or disclaimer of the subject matter contained therein.

Please **amend** the claims as follows:

1. (Twice amended) A substantially purified nucleic acid molecule, said nucleic acid molecule capable of specifically hybridizing, under conditions of 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, to